

RAW SEQUENCE LISTING

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Application Serial Number: 10/SOS,474A
Source: PCT
Date Processed by STIC: 3-22-05

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PCT

RAW SEQUENCE LISTING

DATE: 03/22/2005

PATENT APPLICATION: US/10/505,474A

TIME: 09:58:48

Input Set : A:\10-505474.txt

Output Set: N:\CRF4\03222005\J505474A.raw

3 <110> APPLICANT: Tsukamoto, Akira
 4 Nakagame, Seiji
 5 Kabuto, Mari
 6 Sugiura, Jun
 7 Sakaguchi, Hisako
 8 Furujo, Atsushi
 10 <120> TITLE OF INVENTION: Cellulolytic enzyme gene and use thereof
 12 <130> FILE REFERENCE: 04853-0118-00000
 14 <140> CURRENT APPLICATION NUMBER: US 10/505,474A
 16 <141> CURRENT FILING DATE: 2004-08-24
 18 <150> PRIOR APPLICATION NUMBER: PCT/JP03/02058
 20 <151> PRIOR FILING DATE: 2003-02-25
 22 <160> NUMBER OF SEQ ID NOS: 52
 24 <170> SOFTWARE: PatentIn Ver. 3.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 3420
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Coriolus hirsutus
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 34 tgcccggccat gaagttcaag agtctcctgt tgtccgtggt gccgttggtc ggctctggta 180
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 43 tgcacatgtg cgtacctcac attacgtatg acgtctccaa ctaaacctct tcacagcctg 720
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Cpg. (6)

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58 acttctccac cgccagcgga tggccgagca gctggaccaaa ccaccagccg ttcaccaaca 1620
59 agctgaagca gcgctctgccg agcacagacc acccctccac cgacggccag cgctacctcg 1680
60 aacagtccgc gaacgctcgtc cagcagctgc tccagagcca gggctaccgg caggtcacga 1740
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82 gatgtgctcc aacctctggg tgggcgcccgc gaagatcggc acaagcccgt ccacggccgt 3060
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84 tcttcccgtg cctccgctg acgcggcctt cctgcagttc atcgctgatg cgtccatcat 3180
85 cccgtctctg ccggtcggga acccgagggg cctgctcatg tctgcggccg agcaggccgt 3240
86 gtcgaagatc ctgcgctcg ccggaggacc gtgaggcagg gggttcaaaa gcatttgag 3300
87 cgctgctatg gtagaccatg aagcgggatg ggtcctgtcg atatgagaca cgatgtatat 3360
88 attatatatt ctgcacggtt ttcttcttcc tggaagcctg atgaggctct cgacgtgcc 3420

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91 <210> SEQ ID NO: 2

92 <211> LENGTH: 768

93 <212> TYPE: PRT

94 <213> ORGANISM: Coriolus hirsutus

96 <400> SEQUENCE: 2.

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101           20           25           30
103 Val Phe Asp Gly Val Thr Asp Pro Val His Ser Val Thr Gly Ile
104           35           40           45
106 Val Leu Pro Gln Ala Ala Ser Ser Ser Glu Phe Ile Gly Glu Ile Val
107           50           55           60
109 Ala Pro Asn Asp Ala Gln Trp Ile Gly Leu Ala Leu Gly Gly Ala Met
110           65           70           75           80
112 Ile Gly Asp Leu Leu Leu Val Ala Trp Pro Tyr Glu Asn Lys Ile Ile

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116				100				105					110			
118	Gly	Pro	Thr	Ile	Thr	Thr	Leu	Pro	Ser	Ser	Ser	Ile	Asn	Ser	Thr	His
119			115					120					125			
121	Trp	Lys	Phe	Val	Phe	Arg	Cys	Gln	Asn	Cys	Thr	Ser	Trp	Asp	Gly	Gly
122		130					135					140				
124	Ser	Ile	Asp	Pro	Ser	Gly	Thr	Gly	Val	Phe	Ala	Trp	Ala	Tyr	Ser	Asn
125	145					150				155						160
127	Val	Ala	Val	Asp	Thr	Pro	Ala	Asp	Pro	Asn	Ser	Ser	Phe	Ala	Glu	His
128				165					170						175	
130	Thr	Asp	Phe	Gly	Phe	Phe	Gly	Val	Asn	Phe	Pro	Asp	Ala	Gln	Asn	Ser
131			180						185					190		
133	Asn	Tyr	Gln	Ser	Tyr	Leu	Gln	Gly	Asn	Ala	Gly	Thr	Pro	Pro	Pro	Thr
134			195					200					205			
136	Ser	Val	Pro	Ser	Gly	Pro	Ser	Ser	Thr	Thr	Thr	Thr	Thr	Thr	Gly	Pro
137		210					215						220			
139	Ala	Thr	Ala	Thr	Pro	Phe	Asp	Tyr	Ile	Val	Val	Gly	Ala	Gly	Pro	Gly
140	225					230					235					240
142	Gly	Leu	Ile	Ala	Ala	Asp	Arg	Leu	Ser	Glu	Ala	Gly	Lys	Lys	Val	Leu
143				245						250					255	
145	Leu	Leu	Glu	Arg	Gly	Gly	Pro	Ser	Thr	Ala	Glu	Thr	Gly	Gly	Thr	Tyr
146			260						265					270		
148	Asp	Val	Pro	Trp	Ala	Lys	Ser	Ala	Asn	Leu	Thr	Lys	Phe	Asp	Val	Pro
149		275						280					285			
151	Gly	Leu	Phe	Glu	Thr	Leu	Phe	Thr	Asp	Thr	Asn	Pro	Phe	Trp	Trp	Cys
152		290					295				300					
154	Lys	Asp	Thr	Asn	Phe	Phe	Ala	Gly	Cys	Ile	Leu	Gly	Gly	Gly	Thr	Thr
155	305					310					315					320
157	Val	Asn	Gly	Ala	Leu	Tyr	Trp	Tyr	Pro	Asn	Asn	Asn	Asp	Phe	Ser	Thr
158				325						330					335	
160	Ala	Ser	Gly	Trp	Pro	Ser	Ser	Trp	Thr	Asn	His	Gln	Pro	Phe	Thr	Asn
161			340						345					350		
163	Lys	Leu	Lys	Gln	Arg	Leu	Pro	Ser	Thr	Asp	His	Pro	Ser	Thr	Asp	Gly
164			355						360					365		
166	Gln	Arg	Tyr	Leu	Glu	Gln	Ser	Ala	Asn	Val	Val	Gln	Gln	Leu	Leu	Gln
167		370					375					380				
169	Ser	Gln	Gly	Tyr	Arg	Gln	Val	Thr	Ile	Asn	Asp	Asp	Pro	Asp	Ser	Lys
170	385					390					395					400
172	Asp	His	Val	Phe	Gly	Tyr	Ser	Ala	Phe	Asp	Phe	Leu	Asn	Gly	Gln	Arg
173				405						410					415	
175	Ala	Gly	Pro	Val	Ala	Thr	Tyr	Phe	Gln	Thr	Ala	Leu	Ala	Arg	Lys	Asn
176			420						425					430		
178	Phe	Val	Tyr	Arg	Asp	Asn	Val	Leu	Val	Thr	Gln	Val	Ile	Arg	Asn	Gly
179			435					440					445			
181	Ser	Thr	Ile	Thr	Gly	Val	Arg	Thr	Asn	Asp	Leu	Thr	Ile	Gly	Pro	Asp
182		450					455					460				
184	Gly	Ile	Val	Pro	Leu	Asn	Pro	Asn	Gly	Arg	Val	Ile	Leu	Ala	Gly	Gly
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188                               485                               490                               495
190 Asp Met Leu Gln Val Val Gln Gly Asn Ala Gln Ala Ala Ala Asn Leu
191                               500                               505                               510
193 Pro Pro Gln Asn Gln Trp Ile Asn Leu Pro Val Gly Gln Ala Val Ser
194                               515                               520                               525
196 Asp Asn Pro Ser Ile Asn Leu Val Phe Thr His Pro Ser Ile Asp Ala
197                               530                               535                               540
199 Tyr Asp Asn Trp Ala Thr Val Trp Ser Asn Pro Arg Gln Ala Asp Ala
200 545                               550                               555                               560
202 Gln Gln Tyr Leu Gln Ser Arg Ser Gly Val Leu Ala Gly Ala Ser Pro
203                               565                               570                               575
205 Lys Leu Asn Phe Trp Arg Ala Tyr Gly Gly Ser Asp Gly Ile Thr Arg
206                               580                               585                               590
208 Tyr Ala Gln Gly Thr Val Arg Pro Gly Ala Ala Ser Val Asn Thr Ser
209                               595                               600                               605
211 Val Ala Tyr Asn Ala Ser Gln Ile Phe Thr Ile Thr Leu Tyr Leu Ser
212                               610                               615                               620
214 Asn Gly Ile Gln Ser Arg Gly Arg Ile Gly Val Asp Ala Ala Leu Asn
215 625                               630                               635                               640
217 Ala Lys Ala Leu Val Asn Pro Trp Leu Thr Asn Ala Val Asp Lys Thr
218                               645                               650                               655
220 Ile Leu Leu Gln Ala Leu His Asp Val Val Ser Thr Leu Asn Asn Val
221                               660                               665                               670
223 Gln Gly Leu Thr Met Ile Thr Pro Asp His Thr Met Thr Ile Glu Gln
224                               675                               680                               685
226 Tyr Val Asp Ala Tyr Asp Pro Ala Thr Met Cys Ser Asn His Trp Val
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229 Gly Ala Ala Lys Ile Gly Thr Ser Pro Ser Thr Ala Val Val Asp Glu
230 705                               710                               715                               720
232 Asn Ala Lys Val Phe Asn Thr Asp Asn Leu Phe Ile Val Asp Ala Ser
233                               725                               730                               735
235 Ile Ile Pro Ser Leu Pro Val Gly Asn Pro Gln Gly Leu Leu Met Ser
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242 <210> SEQ ID NO: 3

243 <211> LENGTH: 3480

244 <212> TYPE: DNA

245 <213> ORGANISM: Coriolus hirsutus

247 <400> SEQUENCE: 3

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250 ggtcttgaac ggtgagcacg acactacgac cgcccgccat gaagctcaag agcctcctgt 180
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258 ccggcgggtct acgacggccc aaccattacc aactcccgt ccagttcggg caactcgacg 660
259 cactggaagt tcgtgtttcg ctgccagaac tgcacatgtg cgtacctcac atttcgtacg 720
260 acgtctccaa ctaaacctct tcacagcctg ggatggcgga agcattgacc cctccggcac 780
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262 cagcttcgcc gagcacaccg actgtaagca atcatctctt aatcccgggt ccgaatcact 900
263 catggtatat cgcagtcggc ttcttcggcg tcaacttccc cgatgctcag aactcgaact 960
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265 cttccagcac tacgactact actggtccta cggcaactgt gagcgcttcc acttcactgt 1080
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304 ggtggaccct gaagcgggat ggggttctgtc gatatgagac acgatgtaat attatattct 3420

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 19
Seq#:8; Xaa Pos. 286
Seq#:13; N Pos. 9
Seq#:21; Xaa Pos. 216

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:16,17,22,23,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49
Seq#:50,51,52

VERIFICATION SUMMARY

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L:473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:528 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:272
L:889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:1188 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:1232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:208